

Amendments to the Claims

The listing of the claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claim 1 (currently amended): A homoserine transsuccinylase which possesses at least one mutation as compared with a homoserine transsuccinylase wild-type enzyme and exhibits a reduced sensitivity toward L-methionine or SAM as compared with the wild-type enzyme, with the wild-type enzyme possessing an amino acid sequence which comprises a constituent sequence AspGlyXaaXaaXaaThrGlyAlaPro between positions 90 and 115 and a constituent sequence TyrGlnXaaThrPro between positions 285 and 310, with position 1 of the amino acid sequence being the starting methionine, ~~characterized in that~~ wherein the mutation is an amino acid replacement of the aspartate in the constituent sequence AspGlyXaaXaaXaaThrGlyAlaPro or an amino acid replacement of the tyrosine in the constituent sequence TyrGlnXaaThrPro.

Claim 2 (currently amended): A homoserine transsuccinylase as claimed in claim 1, ~~characterized in that~~ wherein it exhibits a resistance toward SAM or L-methionine which is increased (increased K_i) at least 2-fold as compared with that of the wild type.

Claim 3 (currently amended): A homoserine transsuccinylase as claimed in claim 1 ~~or 2, characterized in that,~~ wherein it contains one of the mutations listed in Table 1.

Claim 4 (currently amended): A metA allele which encodes a homoserine transsuccinylase as claimed in ~~one of claims 1 to 3~~ claim 1.

Claim 5 (currently amended): A plasmid, ~~characterized in that~~ wherein it contains a metA allele as claimed in claim 4 together with a promoter.

Claim 6 (currently amended): A microorganism strain, ~~characterized in that~~ wherein it contains a feedback-resistant metA allele as claimed in claim 4.

Claim 7 (currently amended): A microorganism strain as claimed in claim 6, ~~characterized in that~~ wherein it is a Gram-negative bacterial strain, preferably E. coli.

Claim 8 (currently amended): A method for preparing L-methionine or SAM by culturing a microorganism strain as claimed in claim 6 or 7.